General Description References Comments Links Keywords Sequence

General information

Entry name	ATPG_HAEIN
Accession number	P43716
Created	Rel. 32, 1-NOV-1995
Sequence update	Rel. 32, 1-NOV-1995
Annotation update	Rel. 40, 16-OCT-2001

Description and origin of the Protein

Description	ATP SYNTHASE GAMMA CHAIN (EC 3.6.3.14).
Gene name(s)	ATPG OR HI0480.
Organism source	Haemophilus influenzae.
Taxonomy	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus.
NCBI TaxID	727

References

[1] Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A., Kirkness,E.F., Kerlavage,A.R., Bult,C.J., Tomb,J.-F., Dougherty,B.A., Merrick,J.M., McKenney,K., Sutton,G., Fitzhugh,W., Fields,C.A., Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.-I., Glodek,A., Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E., Cotton,M.D., Utterback,T.R., Hanna,M.C., Nguyen,D.T., Saudek,D.M., Brandon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L., Geoghagen,N.S.M., Gnehm,C.L., McDonald,L.A., Small,K.V., Fraser,C.M., Smith,H.O., Venter,J.C.,
Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
(1995) *Science* **269**:496

Position SEQUENCE FROM N.A.

	Comments	STRAIN=RD / KW20 / ATCC 51907;
	Medline	95350630
	PubMed	7542800

Comments

FUNCTION	PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.
SUBUNIT	F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
SIMILARITY	BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.

Copyright

Database cross-references

EMBL	U32730; AAC22138.1; -.
HSSP	P05631; 1BMF.
TIGR	HI0480; -.
InterPro	IPR000131; ATPase_gamma.
Pfam	PF00231; ATP-synt; 1.
PRINTS	PR00126; ATPASEGAMMA.
PROSITE	PS00153; ATPASE_GAMMA; 1.

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome;

Sequence information

Length: 289 aa, molecular weight: 32069 Da, CRC64 checksum: 622CBA682F37FD00

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KGISFFRSFG FNIKGQLSGL GDTPALEELI GVANTMFDAY RNGEIDAVYI AYNKFVNTMS     180
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General Description References Comments Links Keywords Sequence

ATP synthase gamma subunit

Accession	IPR000131; (ATPase_gamma) matches 100 proteins
FullName	ATP synthase gamma subunit
Type	Domain
Signatures	PRINTS: PR00126 *ATPASEGAMMA* PROSITE: PS00153 *ATPASE_GAMMA* PFAM: PF00231 *ATP-synt*
Molecular Function	hydrogen-transporting two-sector ATPase (GO:0003936)
Biological Process	hydrogen transport (GO:0006818)
Cellular Component	membrane (GO:0016020)
Abstract	ATP synthase (proton-translocating ATPase) [EC:3.6.1.34] [1, 2] is a component of the cytoplasmic membrane of eubacteria, the inner membrane of mitochondria, and the thylakoid membrane of chloroplasts. The ATPase complex is composed of an oligomeric transmembrane sector, called CF(0), and a catalytic core, called coupling factor CF(1). The former acts as a proton channel; the latter is composed of five subunits, alpha, beta, gamma, delta and epsilon. Subunit gamma is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex. The best conserved region of the gamma subunit [3] is its C-terminus which seems to be essential for assembly and catalysis.
Examples	P36542 P00837 P29790 View Signature matches on the examples
	1. Futai,M., Noumi,T., Maeda,M., ATP synthase (H+-ATPase) - Results by combined

References	biochemical and molecular biological approaches. (1989) *Annu. Rev. Biochem.* **58**: 111-136 [MEDLINE:89372792] [PUB00000063] 2. Senior,A.E., ATP synthesis by oxidative phosphorylation. (1988) *Physiol. Rev.* **68**: 177-231 [MEDLINE:88097736] [PUB00004515] 3. Futai,M., Maeda,M., Miki,J., Mukohata,Y., The gamma-subunit of ATP synthase from spinach chloroplasts - primary structure deduced from the cloned CDNA sequence. (1988) *FEBS Lett.* **232**: 221-226 [MEDLINE:88211863] [PUB00001558]
Database links	BLOCKS:IPB000131; PDOC:PDOC00138;
Matches	Table all Graphical all

Related Articles by NCBI

Whole-genome random s quencing and ass mbly of Haemophilus influenzae Rd.

Fleischmann,R D. , Adams,M D. , White,O. , Clayton,R A. , Kirkness,E F. , Kerlavage,A R. , Bult,C J. , Tomb,J F. , Dougherty,B A. , Merrick,J M.

Johns Hopkins University School of Medicine, Baltimore, MD 21205, USA.

An approach for genome analysis based on sequencing and assembly of unselected pieces of DNA from the whole chromosome has been applied to obtain the complete nucleotide sequence (1,830,137 base pairs) of the genome from the bacterium Haemophilus influenzae Rd. This approach eliminates the need for initial mapping efforts and is therefore applicable to the vast array of microbial species for which genome maps are unavailable. The H. influenzae Rd genome sequence (Genome Sequence DataBase accession number L42023) represents the only complete genome sequence from a free-living organism.

Publication Type:
Journal Article

Substances:
Bacterial Proteins
DNA, Bacterial
RNA, Bacterial
RNA, Ribosomal

Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

Fleischmann,R D. , Adams,M D. , White,O. , Clayton,R A. , Kirkness,E F. , Kerlavage,A R. , Bult,C J. , Tomb,J F. , Dougherty,B A. , Merrick,J M.

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Substances:
Bacterial Proteins
DNA, Bacterial
RNA, Bacterial
RNA, Ribosomal

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SV   AR089428.1
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DT   12-SEP-2000 (Rel. 65, Last updated, Version 1)
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OS   unidentified
OC   unclassified.
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RA   Bergeron M.G., Picard F.J., Ouellette M., Roy P.H.;
RT   "Species-specific and universal DNA probes and amplification primers to
RT   rapidly detect and identify common bacterial pathogens and associated
RT   antibiotic resistance genes from clinical specimens for routine diagnosis
RT   in microbiology laboratories";
RL   Patent number US5994066-A/187, 30-NOV-1999.
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RA   Kerlavage A.R., Bult C.J., Tomb J., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F.,
RA   Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.,
RA   Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D.,
RA   Fritchman J.L., Fuhrmann J.L., Geoghagen N.S., Gnehm C.L., McDonald L.A.,
RA   Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd";
RL   Science 269(5223):496-512(1995).
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RA   Tatusov R.L., Mushegian A.R., Bork P., Brown N.P., Hayes W.S.,
RA   Borodovsky M., Rudd K.E., Koonin E.V.;
RT   "Metabolism and evolution of Haemophilus influenzae deduced from a
RT   whole-genome comparison with Escherichia coli";
RL   Curr. Biol. 6(3):279-291(1996).
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RL   The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD
RL   20850, USA
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RA   White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
RT   ;
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RL   The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD
RL   20850, USA
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RN   [5]
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RA   Hickey E., Dodson R., Gwinn M.;
RT   ;
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RL   The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD
RL   20850, USA
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